Figure 3:

Clustal W alignment of precited amino acid sequences of SCS0009 with SV1 and SV2

SCS0009 SV1-ORF		MPSGCRCLHLV	CLLCILGAPGQPVRA
SV2-ORF			
SCS0009 SV1-ORF SV2-ORF	#DDCSSHCDLAHGCCAPDGSCRCDPGWEGLH	MPGCQHGTC MPGCQHGTC	HQPWQCICHSGWAGK HQPWQCICHSGWA HQPWQCICHSGWA ******
	<u>#</u>	<u>#</u>	## AGPCEQAGSPCRNGG
SCS0009			
SV1-ORF	FCDKDEHICTTQSPCQNGGQCMYDGGGEYH		
SV2-ORF	DEHICTTQSPCQNGGQCMYDGGGEYH	CVCLPGFHGRDCERK	AGPCEQAGSPCRNGG
SCS0009 SV1-ORF	QCQDDQGFALNFTCRCLVGFVGARCEVNVD	DCLMRPCANGATCLD	GINRFSCLCPEGFAG
SV2-ORF	QCQDDQGFALNFTCRCLVGFVGARCEVNVD QCQDDQGFALNFTCRCLVGFVGARCEVNVD	DCLMRPCANGATCLD	GINRFSCLCPEGFAG
DVZ OILL	**************************************	*************	GINRESCLCPEGEAG *******
SCS0009	RFCTINLDDCASRPCQRGARCRDRVHDFDC	LCPSGYGGKTCELVL	PVPDPPTTVDTPLGP
SV1-ORF SV2-ORF	RFCTINLDDCASRPCQRGARCRDRVHDFDC	LCPSGYGGKTCELVL	PVPDPPTTVDTPLGP
2AN-OKE	RFCTINLDDCASRPCQRGARCRDRVHDFDC	LCPSGYGGKTCELVL	PVPDPPTTVDTPLGP ********
SCS0009	TSAVVVPATGPAPHSAGAGLLRISVKEVVR	RQEAGLGEPSLVALV	VFGALTAALVLATVL
SV1-ORF	TSAVVVPATGPAPHSAGAGLLRISVKEVVR	RQEAGLGEPSLVALV	VFGALTAALVLATVL
SV2-ORF	TSAVVVPATGPAPHSAGAGLLRISVKEVVR	RQEAGLGEPSLVALV	VFGALTAALVLATVL
	*********	******	******
SCS0009	LTLRAWRRGVCPPGPCCYPAPHYAPACQDQ	ECQVSMLPAGLPLPR	DLPPEPGKTTAL.
SV1-ORF	LTLRAWRRGVCPPGPCCYPAPHYAPACQDQ	ECQVSMLPAGLPLPR	DLPPEPGKTTAL.
SV2-ORF	LTLRAWRRGVCPPGPCCYPAPHYAPACQDQ ***********************************	ECOVSMLPAGLPLPR	DLPPEPGKTTAL.

above amino acids XY = exon boundaries.

In the translation, the SV1 and SV2 sequences are shown representing the longest ORF available.

The predicted signal peptide of SCS0009 is shown highlighted in yellow underlined.

The SV1 and SV2 longest ORFs do not contain predicted signal peptides.

Figure 3:
Clustal W alignment of precited amino acid sequences of SCS0009 with SV1 and SV2

		VID G G G G G T VI I	##
SCS0009		MPSGCRCLHL	VCLLCILGAPGQPVRA
SV1-ORF			
SV2-ORF			
	#		
SCS0009	DDCSSHCDLAHGCCAPDGSCRCDPGWEG	SLHCERCVRMPGCQHGT	CHQPWQCICHSGWAGK
SV1-ORF		MPGCQHGT	CHQPWQCICHSGWAGK
SV2-ORF		MPGCQHGT	CHQPWQCICHSGWA

	#	#	##
SCS0009	FCDK	GFHGRDCER	KAGPCEQAGSPCRNGG
SV1-ORF	FCDKDEHICTTQSPCQNGGQCMYDGGGE		
SV2-ORF	DEHICTTQSPCQNGGQCMYDGGGE	EYHCVCLPGFHGRDCER	KAGPCEQAGSPCRNGG
	*************	*****	*****
sCS0009	QCQDDQGFALNFTCRCLVGFVGARCEVN		
SV1-ORF	QCQDDQGFALNFTCRCLVGFVGARCEVI	NVDDCLMRPCANGATCL	DGINRFSCLCPEGFAG
SV2-ORF	QCQDDQGFALNFTCRCLVGFVGARCEVI	NVDDCLMRPCANGATCL	DGINRFSCLCPEGFAG
	*************	*****	*****
SCS0009	RFCTINLDDCASRPCQRGARCRDRVHD		
SV1-ORF	RFCTINLDDCASRPCQRGARCRDRVHDI		
SV2-ORF	RFCTINLDDCASRPCQRGARCRDRVHDI		
SCS0009	TSAVVVPATGPAPHSAGAGLLRISVKEV	/VRRQEAGLGEPSLVAL	VVFGALTAALVLATVL
SV1-ORF	TSAVVVPATGPAPHSAGAGLLRISVKEV		
SV2-ORF	TSAVVVPATGPAPHSAGAGLLRISVKEV	VVRRQEAGLGEPSLVAL	VVFGALTAALVLATVL
	**************	*****	*****
SCS0009	LTLRAWRRGVCPPGPCCYPAPHYAPAC	~ ~ ~	
SV1-ORF	LTLRAWRRGVCPPGPCCYPAPHYAPAC		
SV2-ORF	LTLRAWRRGVCPPGPCCYPAPHYAPAC		
	*******	******	*****

above amino acids = exon boundaries.

In the translation, the SV1 and SV2 sequences are shown representing the longest ORF available.

The predicted signal peptide of SCS0009 is underlined. The SV1 and SV2 longest ORFs do not contain predicted signal peptides.

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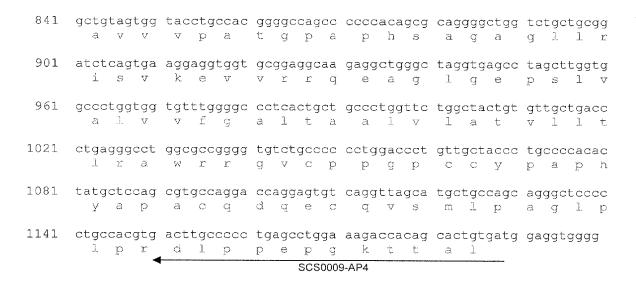
Figure 23

Nucleotide sequence with translation of SCS0009-SV5 PCR product indicating the positions of the SCS0009-AP1, -AP2, -AP3 and -AP4 primers used to generate the SCS0009 sequence.

				SCS0009-AP1		
1	tccatccgtc	cgtccctcct	ggggccggcg ct	gaccatgc	ccagcggctg	ccgctgcctg
					p s g	
61	catctcgtgt	gcctgttgtg	cattctgggg gc	tcccggtc	agcctgtccg	agccgatgac
	h l v	c I I	c i l g	a p g	d b A	radd
121	taasaataaa	agt at agast	aaaaaaaaaa ta	at at a a a a	a+aaaaaa+a	at a se a set est
121			ggcccacggc tgc			
	~ ~ ~ ~	ii G C	a n g	u u a	p d g	scrc
181	gacccgggct.	aaasaaaact	gcactgtgag cg	ctatataa .	agatacctaa	ctaccaacac
			l h c e			
	- w	2				9 - 1 -

241	ggtacctgcc	accagccatg	gcagtgcatc tg	ccacagtg -	gctgggcagg	caagttctgt
			w q c i		g wa	g k f c
					45	SCS0009-AP2
301	gacaaagatg	aacatatctg	taccacgcag to	cacatgae .		
	<u>a k</u> a	e n i	c t t q	s p c	q n g	g q c m
					SCS0009-	AP3
361	tatgacgggg	acaataaata	ccattgtgtg tg	cttaccac	acttccataa	acataactac
			y h c v	79	g f h	grdcgaege
		<i></i>	ad.	<u> </u>		
421			tgaacaggca gg			cgggcagtgc
	e r k	agp	c e q a	g s p	c r n	g g q c
407						
481			tctcaacttc acc			
	q a a	q g i	aln f	t c r	c T A	g f v g
541	accaactata	2001222101	ggatgaetag et	astagaaa	attataata	~~+~~~~
247			ggatgactgc ctc v d d c			n q a t
	a 1 0	C V 11	v a a c .	- 11k d-	p c a	n y a c
601	taccttaaca	gcataaaccg	cttctcctgc ct	etateeta a	agggctttgc	tagacacttc
	c 1 d	g i n	r f s c	1 c p	e a f	a g r f
		~		in the same of the	¹	J
661			ctgtgccage cg			ccgctgtcgg
	c t i	n 1 d	dcas:	r p c	q r g	arcr
721			etgeetetge ce			
	d r v	h d f	d c l c 1	o s g	ъ a a	k t c e
781	a++ a+ a++ a	at at asses	00000000000	o at an		
/ O T	l w 1	orgreecaga	cccccaacc acc	aguggaca (cccctctagg	gcccacctca
	.i. V .i.	b A b	d p p t	L V Q	r b T	g p t s

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<u>Underlined Sequence (positions 308-400)</u> <u>in grey</u> = bases not present in SCS0009 prediction

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Figure 23

Nucleotide sequence with translation of SCS0009-SV5 PCR product indicating the positions of the SCS0009-AP1, -AP2, -AP3 and -AP4 primers used to generate the SCS0009 sequence.

			SCS0009-A	.P1
1	tccatccgtc	egteceteet	ggggccggcg ctgaccatgc ccagcggc	tg ccgctgcctg
			m p s g	c r c l
61	catctcgtgt	gcctgttgtg	cattetgggg geteceggte ageetgte	cg agccgatgac
	h l v	c 1 1	cilgapg qp v	radd
121	tgcagctccc	actgtgacct	ggcccacggc tgctgtgcac ctgacggc	tc ctgcaggtgt
	C S S	h c d	lahgccapdo	
101	~~~~~~~			
181			gcactgtgag cgctgtgtga ggatgcctl h c e r c v r m g	gg ctgccagcac · g c q h
	a b A		atin is is the same to the sam	, 9 6 4 11
241			gcagtgcatc tgccacagtg gctgggca	
	g t c	11 4 b	wqcichsgwa	g k f c SCS0009-AP2
	***************************************			3C30009-AP2
301			taccacgcag tececetgee agaatgga	
	_ a k a	e h i	cttq spc qn g	g q c m
			SCSC	009-AP3
361	tatgacgggg	gcggtgagta	ccattgtgtg tgcttaccag gcttccat	gg gcgtgactgc
	y d g	g g e	y h c v c l p g f h	g r d c
421	gagcgcaagg	ctggaccctg	tgaacaggca ggctccccat gccgcaat	gg cgggcagtgc
	e r k	a g p	ceqagspcr	ggqc
481	caddacdacc	agggetttge	totcaactto acgtgccgct gcttggtg	aa atttataaat
401	q d d	agggettege	a l n f t c r c l v	gg ceeegeggge · a f v a
	-			, , , , , , , , , , , , , , , , , , ,
541			ggatgactgc ctgatgcggc cttgtgct	
	a r c	e v n	vddc 1 m r pca	ngat
601	tgccttgacg	gcataaaccg	ctteteetge etetgteetg agggettt	gc tggacgcttc
	c l d	gin	r f s c l c p e g f	agr f
661	+~~~~~	5.5.5± 0.5.5± 0.5		
661	c t i	n 1 d	ctgtgccagc cgcccatgcc agagagggd d c a s r p c q r g	gc ccgctgtcgg - a r c r
				sass and the
721			etgeetetge eccagtgget atggtgge	
	d r v	h d f	dclcpsgygg	k t c e
781	cttqtcttac	ctgtcccaga	cccccaacc acagtggaca ccctcta	gg gcccacctca
	1 v 1	p v p	d p p t t v d t p l	gpts

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Underlined Sequence (positions 308-400)= bases not present in SCS0009 prediction